

Cancelled  
per #18/p

SEQUENCE LISTING

<110> PARANHOS-BACCALA, Glaucia



KOMURIAN-PRADEL, Florence

BEDIN, Frederic

SODOYER, Mireille

OTT, Catherine

MALLET, Francois

PERRON, Herve

MANDRAND, Bernard

<120> RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR, ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES

<130> 103514

<140> US/09/319,156

<141> 1999-11-02

<150> PCT/FR98/01460

<151> 1998-07-07

<150> FR/97/08816

<151> 1997-07-07

<160> 45

<170> PatentIn version 3.0

<210> 1

<211> 34

<212> DNA

<213> MSRV

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34

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30

<210> 3

<211> 30

<212> DNA

<213> MSRV

<400> 3

ccaatagcca gaccattata tacactaatt

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<210> 4

<211> 310

<212> DNA

<213> MSRV

<400> 4

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agccactgag gaaggaaaaa tactttcacc tgcagctaac caacagaaat tacttaaac 180

ccttcaccaa accttccact taggcattga tagcacccat cagatggcca aattattatt 240

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aagaaataat 310

<210> 5

<211> 103

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<213> MSRV

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<222> (26)..(26)

<223> Xaa = any amino acid

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1 5 10 15

Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His

20 25 30

Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu  
 35 40 45

Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr  
 50 55 60

Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe  
 65 70 75 80

Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys  
 85 90 95

Glu Val Cys Gln Arg Asn Asn  
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<210> 6

<211> 635

<212> DNA

<213> MSRV

<400> 6

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ctggaccggc ctgctagccc atgctccgat gttaatgaca ttgaaggcac ccctcccag 180

gaaatctcaa ctgcacaacc cctactatgc cccaattcag cggaagcag ttagagcgg 240

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attaaatctt gcaactgaaa aaaaaaaaaa aaaaa 635

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<211> 77

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<213> MSRV

<400> 7

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Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser

20 25 30

Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys

35

40

45

Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr

50

55

60

Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser

65

70

75

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<213> MSRV

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32

<210> 9

<211> 1481

<212> DNA

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acgcggcttc ctggaaatat tgatgcccac tcatatagga gtttatctaa gggaaactcc	180
accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg	240
catgcaaata ctcattattg gacagggaaa atgattaatc ctagttgtcc tggaggactt	300
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ctcagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaattattg	1380
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<211> 493

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<222> (39)..(39)

<223> Xaa = any amino acid

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Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser  
20 25 30

Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp  
35 40 45

Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala  
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met  
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys  
85 90 95

Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr  
100 105 110

Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln  
115 120 125

Val	Lys	Glu	Ala	Ile	Ser	Gln	Leu	Thr	Arg	Gly	His	Ser	Thr	Pro	Ser
130						135					140				

Pro	Tyr	Lys	Gly	Leu	Val	Leu	Ser	Lys	Leu	His	Glu	Thr	Leu	Arg	Thr
145					150					155					160

His	Thr	Arg	Leu	Val	Ser	Leu	Phe	Asn	Thr	Thr	Leu	Thr	Arg	Leu	His
			165						170					175	

Glu	Val	Ser	Ala	Gln	Asn	Pro	Thr	Asn	Cys	Trp	Met	Cys	Leu	Pro	Leu
		180						185					190		

His	Phe	Arg	Pro	Tyr	Ile	Ser	Ile	Pro	Val	Pro	Glu	Gln	Trp	Asn	Asn
	195						200					205			

Phe	Ser	Thr	Glu	Ile	Asn	Thr	Thr	Ser	Val	Leu	Val	Gly	Pro	Leu	Val
210						215						220			

Ser	Asn	Leu	Glu	Ile	Thr	His	Thr	Ser	Asn	Leu	Thr	Cys	Val	Lys	Phe
225					230					235					240

Ser	Asn	Thr	Ile	Asp	Thr	Thr	Ser	Ser	Gln	Cys	Ile	Arg	Trp	Val	Thr
			245						250					255	

Pro	Pro	Thr	Arg	Ile	Val	Cys	Leu	Pro	Ser	Gly	Ile	Phe	Phe	Val	Cys
			260					265					270		

Gly	Thr	Ser	Ala	Tyr	His	Cys	Leu	Asn	Gly	Ser	Ser	Glu	Ser	Met	Cys
		275					280							285	

Phe	Leu	Ser	Phe	Leu	Val	Pro	Pro	Met	Thr	Ile	Tyr	Thr	Glu	Gln	Asp
290						295					300				

Leu	Tyr	Asn	His	Val	Val	Pro	Lys	Pro	His	Asn	Lys	Arg	Val	Pro	Ile
305					310					315					320

Leu	Pro	Phe	Val	Ile	Arg	Ala	Gly	Val	Leu	Gly	Arg	Leu	Gly	Thr	Gly
					325				330					335	

Ile	Gly	Ser	Ile	Thr	Thr	Ser	Thr	Gln	Phe	Tyr	Tyr	Lys	Leu	Ser	Gln
			340					345					350		

Glu	Ile	Asn	Gly	Asp	Met	Glu	Gln	Val	Thr	Asp	Ser	Leu	Val	Thr	Leu
		355					360					365			

Gln	Asp	Gln	Leu	Asn	Ser	Leu	Ala	Ala	Val	Val	Leu	Gln	Asn	Arg	Arg
	370					375					380				

Ala	Leu	Asp	Leu	Leu	Thr	Ala	Lys	Arg	Gly	Gly	Thr	Cys	Leu	Phe	Leu
385					390					395					400

Gly	Glu	Glu	Arg	Cys	Tyr	Tyr	Val	Asn	Gln	Ser	Arg	Ile	Val	Thr	Glu
				405					410					415	

Lys	Val	Lys	Glu	Ile	Arg	Asp	Arg	Ile	Gln	Cys	Arg	Ala	Glu	Glu	Leu
			420					425				430			

Gln	Asn	Thr	Glu	Arg	Trp	Gly	Leu	Leu	Ser	Gln	Trp	Met	Pro	Trp	Val
		435					440					445			

Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Leu Phe  
450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile  
465 470 475 480

Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro  
485 490

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<211> 32

<212> DNA

<213> MSRV

<400> 11

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32

<210> 12

<211> 1329

<212> DNA

<213> MSRV

<220>

<221> misc\_feature

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<223> n = a, g, c or t/u

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aatttgagat cgaatataat gtagagcaga ggaccttcaa aacactgcac cctggggcct	180
cctcagccaa tggatgccct ggactctccc cttcttagga cctctagcag ctataatatt	240
tttactcttc tttggaccct gtatcttcaa cttccttggt aagtttgtct cttccagaat	300
tgaagctgta aagctacaaa tagttcttca aatggaaccc cagatgcagt ccatgactaa	360
aatctaccgt ggacccttg accggcctgc tagactatgc tctgatgtta atgacattga	420
agtcaccct cccgaggaaa tctcaactgc acaacccta ctacactcca attcagtagg	480
aagcagttag agcagttgtc agccaacctc cccaacagta cttgggtttt cctgttgaga	540
gggtggactg agagacagga ctagctggat ttcttaggct gactaagaat ccnaagcct	600
anctgggaag gtgaccgcat ccattcttaa acatggggct tgcaacttag ctacaccccg	660
accaatcaga gagctcacta aaatgctaata caggcaaaaa caggaggtaa agcaatagcc	720

aatcatctat tgcctgagag cacagcggga aggacaagga ttgggatata aactcaggca	780
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cactctattt cactctatta aatcatgcaa ctgcactctt ctggtccgtg ttttttatgg	900
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tgggtttgtc ctaatagaac tgaacactgg tcaactgggtt ccatggttct cttccatgac	1140
ccacggcttc taatagagct ataacactca ccgcatggcc caagattcca ttctttggtg	1200
tctgtgaggc caagaacccc aggtcagaga angtgaggct tgccaccatt tgggaagtgg	1260
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<222> (26)..(26)

<223> Xaa = any amino acid

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<222> (42)..(42)

<223> Xaa = any amino acid

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<222> (46)..(46)

<223> Xaa = any amino acid

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1

5

10

15

Cys Leu Phe Leu Gly Glu Glu Cys Cys Xaa Tyr Val Asn Gln Ser Gly

20

25

30



Ile Ile Thr Glu Lys Val Lys Glu Ile Xaa Asp Arg Ile Xaa Cys Arg  
35 40 45

Ala Glu Asp Leu Gln Asn Thr Ala Pro Trp Gly Leu Leu Ser Gln Trp  
50 55 60

Met Pro Trp Thr Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Phe  
65 70 75 80

Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Phe Leu Val Lys Phe Val  
85 90 95

Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Ile Val Leu Gln Met Glu  
100 105 110

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg  
115 120 125

Pro Ala Arg Leu Cys Ser Asp Val Asn Asp Ile Glu Val Thr Pro Pro  
130 135 140

Glu Glu Ile Ser Thr Ala Gln Pro Leu Leu His Ser Asn Ser Val Gly  
145 150 155 160

Ser Ser

<210> 14

<211> 21

<212> DNA

<213> MSRV

<400> 14

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21

<210> 15

<211> 21

<212> DNA

<213> MSRV

<400> 15

catgtcacca ggggtggaata g

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<210> 16

<211> 758

<212> DNA

<213> MSRV

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atgttccttc aggagaacaa agaacaggcc attacccagg ggaagactgg caactagatt	180
ttacccacat ggccaaatgt cagggatttc agcatctact agtctgggca gatactttca	240
ctggttgggt ggagtcttct ccttgtagga cagaaaagac ccaagaggta ataaaggcac	300
taatgaaata attcccagat ttggacttcc ccaggatta cagggtgaca atggccccgc	360
tttcaaggct gcagtaacct agggagtatc ccagggtgta ggcatacaat atcacttaca	420
ctgtgcctgg aggccacaat cctccagaaa agtcaagaaa atgaatgaaa cactcaaaga	480
tctaaaaaag ctaacccaag aaaccacat tgcattgacct gttctgttgc ctataacctt	540
actaagaatc cataactatc ccccaaaaag caggacttag ccatacgag atgctatatg	600
gatggccttt cctaaccaat gaccttgtgc ttgactgaga aatggccaac ttagttgcag	660
acatcacctc cttagccaaa tatcaacaag ttctttaaac atcacaggga acctgtcccc	720
gagaggaggg aaaggaacta ttccaccctg gtgacatg	758

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<212> DNA

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25

<210> 18

<211> 26

<212> DNA

<213> MSRV

<400> 18

ggacaggaaa gtaagactga gaaggc

26

<210> 19

<211> 26

<212> DNA

<213> MSRV

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cctagaacgt attctggaga attggg

26

<210> 20

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<212> DNA

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tggtctctcaa tggtcaaaca tacccg

26

<210> 21

<211> 1511

<212> DNA

<213> MSRV

<400> 21

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atttatattc ttctgcagta ccgcctggcc acaatatcct cttcaaggga gagaaacctg 120

gcttcctgag ggaagtataa attataacat catcttacag ctagacctct tctgtagaaa 180

ggagggcaaa tggagtgaag tgccatatgt gcaaactttc ttttcattaa gagacaactc 240

acaattatgt aaaaagtgtg gtttatgccc tacaggaagc cctcagagtc cacctcccta 300

ccccagcgtc ccctccccga ctccttcttc aactaataag gacccccctt taacccaaac 360

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tataatgtta ctactaaatc agacactaac cccaaatgag agaagtgccg ctgtaactgc	660
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<211> 352

<212> PRT

<213> MSRV

<400> 22

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Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr

20 25 30

Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr

35 40 45

Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp  
 50 55 60

Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser  
 65 70 75 80

Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser  
 85 90 95

Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn  
 100 105 110

Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly  
 115 120 125

Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu  
 130 135 140

Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro  
 145 150 155 160

Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe  
 165 170 175

Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln  
 180 185 190

Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr  
 195 200 205



Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe  
210 215 220

Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu  
225 230 235 240

Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro  
245 250 255

His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu  
260 265 270

Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met  
275 280 285

Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu  
290 295 300

Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser  
305 310 315 320

Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe  
325 330 335

Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro  
340 345 350

<210> 23

<211> 30

<212> DNA

<213> MSRV

<400> 23

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30

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<213> MSRV

<400> 25

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1

5

10

15

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
20 25 30

Ile Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr  
35 40 45

Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln  
50 55 60

Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn  
65 70 75 80

Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys  
85 90 95

Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn  
100 105 110

Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln  
115 120 125

Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr  
130 135 140

Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys  
145 150 155 160

Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro  
165 170 175

Leu Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val  
180 185 190

Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys  
195 200 205

Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly  
210 215 220

Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln  
225 230 235 240

Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu  
245 250 255

Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr  
260 265 270

Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp  
275 280 285

Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His  
290 295 300

Leu Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro  
305 310 315 320

Met Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn  
325 330 335

Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr  
340 345 350

Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys  
355 360 365

Phe Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu  
370 375 380

Pro Lys Leu Ala Ala Ala Leu Glu His His His His His His  
385 390 395

<210> 26

<211> 378

<212> PRT

<213> MSRV

<400> 26

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Leu Glu Arg  
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Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu Arg Lys Lys  
20 25 30

Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr Pro Leu Gln  
35 40 45

Gly	Arg	Glu	Thr	Trp	Leu	Pro	Glu	Gly	Ser	Ile	Asn	Tyr	Asn	Ile	Ile
50						55					60				

Leu	Gln	Leu	Asp	Leu	Phe	Cys	Arg	Lys	Glu	Gly	Lys	Trp	Ser	Glu	Val
65					70					75					80

Pro	Tyr	Val	Gln	Thr	Phe	Phe	Ser	Leu	Arg	Asp	Asn	Ser	Gln	Leu	Cys
				85					90					95	

Lys	Lys	Cys	Gly	Leu	Cys	Pro	Thr	Gly	Ser	Pro	Gln	Ser	Pro	Pro	Pro
			100					105					110		

Tyr	Pro	Ser	Val	Pro	Ser	Pro	Thr	Pro	Ser	Ser	Thr	Asn	Lys	Asp	Pro
		115						120					125		

Pro	Leu	Thr	Gln	Thr	Val	Gln	Lys	Glu	Ile	Asp	Lys	Gly	Val	Asn	Asn
	130					135						140			

Glu	Pro	Lys	Ser	Ala	Asn	Ile	Pro	Arg	Leu	Cys	Pro	Leu	Gln	Ala	Val
145					150					155					160

Arg	Gly	Gly	Glu	Phe	Gly	Pro	Ala	Arg	Val	Pro	Val	Pro	Phe	Ser	Leu
				165					170					175	

Ser	Asp	Leu	Lys	Gln	Ile	Lys	Ile	Asp	Leu	Gly	Lys	Phe	Ser	Asp	Asn
			180						185					190	

Pro	Asp	Gly	Tyr	Ile	Asp	Val	Leu	Gln	Gly	Leu	Gly	Gln	Ser	Phe	Asp
		195					200						205		

Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr Leu Thr Pro  
 210 215 220

Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe Gly Asp Leu  
 225 230 235 240

Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu Glu Arg Thr  
 245 250 255

Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro His Trp Asp  
 260 265 270

Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu Leu Thr Cys  
 275 280 285

Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met Asn Tyr Ser  
 290 295 300

Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu Thr Ala Phe  
 305 310 315 320

Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser Leu Ser Pro  
 325 330 335

Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe Ile Thr Gln  
 340 345 350

Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro Lys Leu Ala  
 355 360 365

Ala Ala Leu Glu His His His His His His

370

375

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<211> 25

<212> DNA

<213> MSRV

<400> 27

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25

<210> 28

<211> 20

<212> DNA

<213> MSRV

<400> 28

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20

<210> 29

<211> 25

<212> DNA



<213> MSRV

<400> 29

ctatgtcctt ttggactggt tgggt

25

<210> 30

<211> 764

<212> DNA

<213> MSRV

<400> 30

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tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca 180

ctgcatgggc caagattcca ttcttggaa tccgtgagac caagaacccc aggtcagaga 240

acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggagc agcccggcac 300

tatcttggga gctctgggag caaggaccgc aggttaacaat ttggtgacca cgaagggacc 360

tgaatccgca accatgaagg gatctccaaa gcaattggaa atgttcctcc caaggcaaaa 420

atgccctaa gatgtattct ggagaattgg gaccaatttg accctcagac agtaagaaaa 480

aaatgactta tattcttctg cagtaccgcc ctggccacga taccctcttc aagggggaga 540  
 aacctggcct cctgagggaa gtataaatta taacaccatc ttacagctag acctgttttg 600  
 tagaaaagga ggcaaatgga gtgaagtgcc atatttacaa actttctttt cattaaaaga 660  
 caactcgcaa ttatgttaac agtgtgattt gtgttcctac acggaagccc tcagattcta 720  
 ctccccaccc ccggcatctc ccttgaatcc ctcccact tatt 764

<210> 31

<211> 800

<212> DNA

<213> MSRV

<400> 31

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 tcaactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca 180  
 ctgcatgggc caagattcca ttcttgga tccgtgagac caagaacccc aggtcagaga 240  
 acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggaagc ggcccggcac 300

tatcttggga gctctgggag caaggacccc caggttaacaa tttggtgacc acgaagggac	360
ctgaatccgc aaccatgaag ggatctccaa agcaattgga aatgttcctc ccaaggcaaa	420
aatgccccta agatgtattc tggagaattg ggaccaatct gaccctcaga cagtaagaaa	480
aaaaatgact tatattcttc tgcagtaccg cctggccacg gatatcctct tcaaggggga	540
gaaacctggc ctcttgaggg aagtataaat tataacacca tcttacagct agacctgttt	600
tgtagaaaag gaggcaaag gagtgaagtg ccatatttac aaactttctt ttcattaaaa	660
gacaactcgc aattatgtaa acagtgtgat ttgtgtccta caggaagccc tcagatctac	720
ctccctaccc cggcattctc ctgactcctt ccccaactaa taaggaccca cttcagccca	780
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<210> 32

<211> 65

<212> PRT

<213> MSRV

<400> 32

Pro	Met	Ala	Ser	Asn	Arg	Ala	Ile	Thr	Leu	Thr	Ala	Trp	Ser	Lys	Ile
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Pro Phe Leu Gly Ile Arg Glu Thr Lys Asn Pro Arg Ser Glu Asn Thr

20

25

30

Arg Leu Ala Thr Met Leu Glu Ala Ala His His His Phe Gly Ser Ser

35

40

45

Pro Pro Leu Ser Trp Glu Leu Trp Glu Gln Gly Pro Gln Val Thr Ile

50

55

60

Trp

65

<210> 33

<211> 26

<212> DNA

<213> MSRV

<400> 33

tcattgcaact gcactcttct ggtccg

26

<210> 34

<211> 28

<212> DNA

<213> MSRV

<400> 34

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28

<210> 35

<211> 28

<212> DNA

<213> MSRV

<400> 35

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28

<210> 36

<211> 31

<212> DNA

<213> MSRV

<400> 36

tcgggtctaa gaggggtactt cctttggtag g

31

<210> 37

<211> 25

<212> DNA

<213> MSRV

<400> 37

ttacgcaggt ctcagggatg agctt

25

<210> 38

<211> 33

<212> DNA

<213> MSRV

<400> 38

cggcagtagc agtcttagta tctgaagcag tta

33

<210> 39

<211> 28

<212> DNA

<213> MSRV

<400> 39

ggtacggagg gtttcatgta gttttgag

28

<210> 40

<211> 1247

<212> DNA

<213> MSRV

<220>

<221> misc\_feature

<222> (1246)..(1246)

<223> n = a, g, c or t/u

<400> 40

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atggctagca tgactggtgg acagcaaag ggtaggatcc tagaacgtat tctggagaat 120

tgggaccaat gtgacactca gacgctaaga aagaacgat ttatattctt ctgcagtacc 180

gcctggccac aatatcctct tcaaggaga gaaacctggc ttcctgaggg aagtataaat 240

tataacatca tcttacagct agacctctt tctagaaagg agggcaaag gagtgaagt 300

ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt 360

ttatgcccta caggaagccc tcagagtcca cctccotacc ccagcgtccc ctccccgact	420
ccttctctcaa ctaataagga ccccccttta acccaaacgg tccaaaagga gatagacaaa	480
ggggtaaaca atgaaccaaa gagtgccaat attccccgat tatgccccct ccaagcagtg	540
agaggaggag aattcggccc agccagagtg cctgtacctt tttctctctc agacttaaag	600
caaattaaaa tagacctagg taaattctca gataaccctg acggctatat tgatgtttta	660
caagggttag gacaatcctt tgatctgaca tggagagata taatgttact actaaatcag	720
acactaacc ccaatgagag aagtgccgct gtaactgcag cccgagagtt tggcgatctt	780
tggtatctca gtcaggccaa caataggatg acaacagagg aaagaacaac tcccacaggc	840
cagcaggcag ttcccagtgt agaccctcat tgggacacag aatcagaaca tggagattgg	900
tgccacaaac atttgctaac ttgcgtgcta gaaggactga ggaaaactag gaagaagcct	960
atgaattact caatgatgtc cactataaca cagggaaagg aagaaaatct tactgctttt	1020
ctggacagac taaggagggc attgaggaag catacctccc tgtcacctga ctctattgaa	1080
ggccaactaa tcttaaagga taagtttate actcagtcag ctgcagacat tagaaaaaac	1140
ttcaaaagtc tgcctaagct tgcggccgca ctcgagcacc accaccacca ccaactgagat	1200
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<210> 41

<211> 1186

<212> DNA

<213> MSRV

<400> 41

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gcctggccac aatatcctct tcaagggaga gaaacctggc ttcctgaggg aagtataaat 180  
tataacatca tcttacagct agacctcttc tgtagaaagg agggcaaag gagtgaagtg 240  
ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt 300  
ttatgcccta caggaagccc tcagagtcca cctccctacc ccagcgtccc ctccccgact 360  
ccttctcaa ctaataagga cccccctta acccaaacgg tccaaaagga gatagacaaa 420  
ggggtaaaca atgaacaaa gagtgccaat attccccgat tatgccccct ccaagcagtg 480  
agaggaggag aattcggccc agccagagtg cctgtacctt tttctctctc agacttaaag 540  
caaattaaaa tagacctagg taaattctca gataaccctg acggctatat tgatgtttta 600  
caagggttag gacaatcctt tgatctgaca tggagagata taatgttact actaaatcag 660

acactaacc	caa	atgagag	aag	tgccgct	gta	actgcag	ccc	gagagtt	tgg	cgatctt	720	
tgg	tatctca	gtc	aggccaa	caat	aggatg	aca	acagagg	aa	agaacaac	tccc	acaggc	780
cag	caggcag	ttccc	agtgt	agac	cctcat	tggg	acacag	aat	cagaaca	tgg	agattgg	840
tgc	cacaaac	attt	gctaac	ttg	ctgcta	gaag	gactga	ggaaa	actag	ga	agaagcct	900
at	gaattact	caat	gatgtc	cact	tataaca	cagg	gaaagg	aagaaa	aatct	tact	gctttt	960
ct	ggacagac	taag	ggaggc	att	gaggaag	cata	ctccc	tgt	cacctga	ctct	attgaa	1020
gg	ccaactaa	tct	taaagga	taag	tttatac	act	cagtcag	ctg	cagacat	tag	aaaaaac	1080
tt	caaaagtc	tgc	ctaagct	tgc	ggccgca	ctc	gagcacc	acc	accacca	ccact	gagat	1140
cc	ggtgcta	aca	aagccccg	aa	aggaagct	ga	ttggctg	gt	ggca			1186

<210> 42

<211> 2030

<212> DNA

<213> MSRV

<400> 42

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gc	ccccctc	cat	gtgctg	taca	accagt	ag	ctcccctt	acca	agagtt	tct	atgaaga	120

acgcggcttc ctggaaatat tgatgccccca tcatatagga gtttatctaa gggaaactcc	180
accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg	240
catgcaaata ctcattattg gacagggaaa atgattaatc ctagttgtcc tggaggactt	300
ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg gggtggaatt	360
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agcacccta gccctacaa aggactagtt ctctcaaac tacatgaaac cctccgtacc	480
catactcgcc tggtgagcct atttaatacc accctcactc ggctccatga ggtctcagcc	540
caaaacccta ctaactgttg gatgtgcctc ccctgcact tcaggccata catttcaatc	600
cctgttcctg aacaatggaa caacttcagc acagaaataa acaccacttc cgttttagta	660
ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt	720
agcaatacta tagacacaac cagctcccaa tgcctcaggt gggtaacacc tcccacacga	780
atagtctgcc taccctcagg aatatttttt gctgtggta cctcagccta tcattgtttg	840
aatggctctt cagaatctat gtgcttcctc tcattcttag tgccccctat gaccatctac	900
actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtaccatt	960
cttccttttg ttatcagagc aggagtgcga ggcagactag gtactggcat tggcagtatc	1020

acaacctcta ctcagttcta ctacaaacta tctcaagaaa taaatgggtga catggaacag 1080  
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 ggagaagaac gctgttatta tgtaatacaa tccagaattg tcaactgagaa agttaagaa 1260  
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tcgagccggc aacggcaacc ccctttgggt cccctccctt tgtatgggcg ctctgttttc 1980

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<210> 43

<211> 2055

<212> DNA

<213> MSRV

<400> 43

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tttgttcgcc atccaccact gctgtttgcc accgtcacag acccgctgct gacttccatc 180

cctttggatc cagcagagtg tccgctgtgc tctgatcca gcacaggcgc ccattgcctc 240

tcccaattgg gctaaaggct tgccattgtt cctgcacagc taagtgcctg gggtcatcct 300

aatcgagctg aacactagtc actgggttcc acggttctct tccatgacct atggcttcta 360

atagagctat aacactcact gcatgggtcca agattccatt ccttggaatc cgtgagacca 420

agaaccccag gtcagagaac acaaggcttg ccaccatgtt ggaagcagcc caccaccatt 480

ttggaagcag cccgccacta tcttgggagc tctgggagca aggaccccag gtaacaattt 540

ggtgaccacg aagggacctg aatccgcaac catgaagga tctccaaagc aatgggaaac	600
gttccccccg aggcaaaaat gccctagaa cgtattctgg agaattggga ccaatgtgac	660
actcagacgc taagaaagaa acgatttata ttcttctgca gtaccgctg gccacaatat	720
cctcttcaag ggagagaaac ctggcttctt gagggaagta taaattataa catcatctta	780
cagctagacc tcttctgtag aaaggagggc aaatggagt aagtgccata tgtgcaaact	840
ttcttttcat taagagacaa ctcacaatta tgtaaaaagt gtggtttatg ccctacagga	900
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tcctttgatc tgacatggag agatataatg ttactactaa atcagacact aaccccaaata	1260
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gccaacaata ggatgacaac agaggaaaga acaactccca caggccagca ggcagttccc	1380
agtgtagacc ctcatggga cacagaatca gaacatggag attggtgcca caaacatttg	1440

ctaacttgcg tgctagaagg actgaggaaa actaggaaga agcctatgaa ttactcaatg	1500
atgtccacta taacacaggg aaaggaagaa aatcttactg cttttctgga cagactaagg	1560
gaggcattga ggaagcatac ctccctgtca cctgactcta ttgaaggcca actaatctta	1620
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ttagtcatgg ccctcaggca agcggacttt ggaggctctg gaaaaggga aagctgggca	1860
aataggaagc ctaatagggc ttgcttccag tgcggtctac aaggacactt taaaaaagat	1920
tgtccaaata gaaataagcc gcccccttgt ccattgccct tacgtcaagg gaatcactgg	1980
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<210> 44

<211> 1197

<212> DNA

<213> MSRV

<400> 44

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gaaggaaaaa tacttttgct ggcagctaac caatggaaat tacttaaaac ccttcagcaa 180  
accttcact taggcattga tagcacccat cagatagcca aatcattatt tactggacca 240  
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cccctgcctt atcgccaagc tccttcagga gaacaagaa caggcaatta cccaagagaa 360  
gactggcaac tagattttat ccacatgcca aaatcacagg gatttcagtg tctactagtc 420  
tgggtagata ctttcactgg ttgggcagag gccctccct gtaggacaga aaagttccaa 480  
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ggtatagaat atcacttaca ctgcacctag aggccacaat cctcagggaa ggttgagaaa 660  
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ttacaaggag cctgtccccg agaggagga aaagaaatat tccaccctgg tgtcatggta 960  
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 ccagtcattt tatctatccc aactgcggtt aaagtggctg gagtggagtc ttggatacat 1080  
 cacactcgaa tcaaaccctg gatactgccg aaggaaccgg aaaatccagg ggacaacgct 1140  
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<210> 45

<211> 1718

<212> DNA

<213> MSRV

<400> 45

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 gaaagaagta gtaaagaaaa aacagtatac cctattcctt taaaagccag ggtaaatttc 180  
 tgtctaccta gccaaaggcat attcttctta tgtggaacat caacctatat ctgcctcccc 240  
 actaactgga caggcaccag aaccttagtc tttctaagtc ccaacattaa cattgcccc 300

ggaaatcaga ccctattggt acctgtcaaa gctaaagtcc gtcagtgcag agccatacaa 360  
 ctaatatccc tatttatagg gttaggaatg gctactgcta caggaactgg aatagccggt 420  
 ttatctactt cattatccta ctaccataca ctctcaaaga atttctcaga cagtttgcaa 480  
 gaaataatga aatctattct tactttacaa tccaattag actctttggc agcaatgact 540  
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